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258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	409.6	57.3	671	175	BG249053	602361828
2	289.6	40.5	2099	192	AK008601	Mus muscu
3	280.8	39.3	906	21	A1529750	u182a02.y
4	245.4	34.3	889	150	BF533715	602073925
5	201.4	28.2	548	16	A1119588	u105c02.y
6	189.8	26.5	529	110	AW012524	u06a07.y
7	175.8	24.6	601	227	AQ371717	RPC111-15
8	162.6	22.7	777	16	A1116747	u28e05.y
9	158.2	22.1	2573	192	AK004971	Mus muscu
10	153.2	21.4	996	21	A1530408	u192f08.y
11	152.8	21.4	1896	192	AK002736	Mus muscu
12	152.1	21.3	923	21	A1529976	u187g04.y
13	151.4	21.2	697	153	BG427192	602494236
14	145.8	20.4	819	16	A1156939	u149c01.y
15	142.1	19.9	909	21	A1528459	u197f08.y
16	138.4	19.4	796	16	A1097842	u40e09.y
17	138.2	19.3	924	21	A1528431	u197d02.y
18	133.1	18.6	954	169	BF780608	602103156
19	133.1	18.6	1096	169	BF788115	602113339
20	132.1	18.5	881	2	AA109874	mm02f06.r
21	128.2	17.9	844	22	A1573962	u166f05.y
22	126.4	17.7	660	146	BF237356	602025029
23	126.2	17.7	595	155	BG562901	602581752
24	125.6	17.6	685	18	A1324412	mm02f06.y
25	123.6	17.3	1059	169	BF784658	602110381
26	123.4	17.3	707	14	AA986985	uc08n04.y
27	119.1	16.6	785	153	BG429706	602493711
28	119.1	16.6	787	153	BG430305	602503209
29	117.1	16.4	688	169	BF782813	602107673
30	116.1	16.2	756	153	BG429801	602494817
31	114.6	16.0	855	169	BF784106	602110061
32	114.6	16.0	954	169	BF787491	602113909
33	114.2	16.0	821	153	BG402643	602465575
34	111.6	15.6	932	148	BF383536	602044428
35	110.4	15.4	901	153	BG400539	602464778
36	109.6	15.3	803	169	BF788917	602104648
37	109.1	15.2	754	19	A1386294	mm75g08.y
38	106.4	14.9	589	16	A1119259	u24d05.y
39	104.2	14.6	665	146	BF236531	602028707
40	103.6	14.5	741	146	BF235182	602026457
41	103.1	14.4	728	153	BG433410	602501120
42	101.8	14.2	884	150	BF533130	602073667
43	101.8	14.2	905	150	BF532101	602073223
44	101.6	14.2	527	17	A1225575	u105f12.y
45	100.4	14.0	457	153	BG412991	ia83d08.y

ALIGNMENTS

RESULT	1
BG249053	
LOCUS	602361828F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4470199 5', 13-FEB-2001
DEFINITION	mRNA sequence.
ACCESSION	BG249053
VERSION	BG249053.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 671)
TITLE	NIH-MGC http://mgc.nci.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM10287 row: h column: 08
High quality sequence stop: 661.

FEATURES

Location/Qualifiers
1..671
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4470199"
/clone_lib="NIH_MGC_89"
/tissue_type="hypernephroma, cell line"
/lab_host="PH10B (phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 206 a 123 c 153 g 189 t
ORIGIN

Query Match 57.3%; Score 409.6; DB 175; Length 671;

Best Local Similarity 95.3%; Pred. No. 3.1e-104;

Matches 509; Conservative 0; Mismatches 14; Indels 11; Gaps 8;

QY 167 tgactcaactcaagccttcgttaattgactacaggaagccttcgtcattgaggaattgag 226

Db 11 TGACTCACTCAAGCCCTTGCTTAA-TGACTACAGGAGCCTTCTGCATGAAA--TTGAGG 67

QY 227 tggctccatgcccacagagcagacagagagagagagagagagagagagagagagag 286

Db 68 TGTCTCATATGCCACAGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126

QY 287 atgtctgcccagccttatcaacctggaatcagttataattataatgattttttgtg 346

Db 127 ATGCTCTGCCAGCCTTATCAACCTGGCAATCAGTTATATAA--TTAATGATTTTGTG 186

QY 347 aataag 406

Db 187 AATAAG 246

QY 407 agaagctacag 466

Db 247 AGAAGCTACAGGAG 306

QY 467 acctgatgctgagtgcttccagtcctctttgtgctcacttagaactct-ctaaga 525

Db 307 ACCTGATGCTGAGTTCCTTGTGAGTCCCTTGTGCTCACTAGATTCTGTGAGGA 366

QY 526 ggcaatgag 583

Db 367 GGCAATATGGAGGAG 426

QY 584 ctatgacag 639

Db 427 CTATGACAG 486

QY 640 ctttcagtttcttcactcttgattcaggattcagcattcatttttgggaa 693

Db 487 CTTTCAGTTTGTGCCACTCTCTGGATTACGATTACGACATTCATCTGTTGGGGA 540

RESULT 2

AK008601

LOCUS

DEFINITION

AK008601 2099 bp mRNA

Mus musculus adult male small intestine cDNA, RIKEN full-length

enriched library, clone:2010321J07, full insert sequence.

HTC

08-FEB-2001

ACCESSION AK008601.1 GI:12842884
 CAP trapper.
 Mus musculus (strain:C57BL/6J) adult male small intestine cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library clone:2010321J07.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CARNINCI, P., SHIBATA, Y., HAYATSU, N., SUGAHARA, Y., SHIBATA, K., CARNINCI, P., KONNO, H., OKAZAKI, Y., MURAMATSU, M. and HAYASHIZAKI, Y.
 High-efficiency full-length cDNA cloning
 Methods Enzymol. 303, 19-44 (1999)
 2 (sites)
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Carninci, P., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20939374
 3 (sites)
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Kikuchi, I., Ishii, Y., Nakamura, S., Hazama, T., Nishine, I., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 4 (sites)
 The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5 (bases 1 to 2099)
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
 FEATURES
 Location/Qualifiers
 1. 2099
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 /strain="C57BL/6J"
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 /sex="male"
 /tissue_type="small intestine"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="adult"
 15. 1619
 /note="putative"
 CDS

[illegible]

BASE COUNT	223 a	186 c	236 g	244 t
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Query Match	34.3%	Score 245.4;	DB 150;	Length 889;
Best Local Similarity	63.2%;	Pred. No. 4.2e-58;		
Matches	448;	Conservative	0;	Mismatches 246; Indels 15; Gaps
Qy	1	atgaggtctgacaaagtcagcttctgtgtattctctcctcgcagctcttctgtgtgctgt	60	
Db	19	ATGGTCTCTGAAAAATGTGTGGCCATTTTTCGTCTGAGCTTTGCTGGCGGGCTGT	78	
Qy	61	ggaattctgtggaagtcctcgtgtgcccctgtgacattgagccattgcttaattgtcaag	120	
Db	79	GGATCTTGACACAGGTCCTCGTGTGGCCCTGTGATATGAGCCACTGGCTGAATCTAAAG	138	
Qy	121	gtcattctagaagagctcattagtgagaggccatgagglaacagctattgactcactcaag	180	
Db	139	ACTATCTTGTAGGAGCTTGGAGCAAGGGCAGGTAACAGTCCTGAAATACCCCA--	196	
Qy	181	ctcttgtaattgactcacagaagccctctgcattgaaatttgagggtggtccatgccca	240	
Db	197	-GTATCATCATAGATCAGAGTAACGTAATCCACTGCACCTTGAGATATATTCCTTTCGTG	255	
Qy	241	caggacaacacagaagaaaatgaaatat-----ttgtgacctagctcctgaatgtc	291	
Db	256	TATGAATCGAGACAGCTGAGAATCGTTTAAATGAGATTGCAAAATCTAGCTGTGAATGTC	315	
Qy	292	tggcaggcttatcaacctggcaatcagttataaaattaaatgattttttgttgaaata	351	
Db	316	ATTCCAAACCTGTCTACTGTGGAGCACCAAAACATTTACAGACTCTTCTTCAAGTA	375	
Qy	352	agagaaactttaaaaatgatgtgagagctttatctacaatcagacacttatgaaagag	411	
Db	376	ACTGGAGATTTGAAAGTATGTAGGAGTG--TATTGTACAAACCAAGAAATTCATGGACAAG	433	
Qy	412	ctacaggaacccaactacagatgaacgcttataacccctgattcccccgtggagacctg	471	
Db	434	CTACGGGATGACAAATATGATGTAGTGTGTTATAGACCTCTGCTTCCCTGTGGAGAGTTG	493	
Qy	472	atggctgagttgcttcacagtccttttgtgctcacacttagaaccttctctaaaggccaat	531	
Db	494	GTGGCAGAGTGCTTTCAGATCCCTTTCGTATACACACTGAGGTTTCAGCATGGCTACTAC	553	
Qy	532	atggagcgaagctgtgggaaacctccagctccacttccctatgtacctgtgcctatgaca	591	
Db	554	ATGGAGAAACACTGTGTGGCCAGCTTCCAAATTCACATCTCGTATGTACCCGGTGTCATTGAGT	613	
Qy	592	ggactaacacagacagaataacctttctggaagag-taaaaattcaalgctttcagtttt	650	
Db	614	GAGCTGACAGACAAATATGACCTTCACAGAGGGTTGAAAAACTATGATGTTTTTCACGTGT	673	
Qy	651	gttccactctggattcaggattacagctatcatcttttgggaagagttt	699	
Db	674	GTTTGAGTACTGTGTCGCCCAATATGACTTGTCTTCTGGGATCAGGTTT	722	
RESULT	5			
LOCUS	A1119588	548 bp	mRNA	EST
DEFINITION	uf05c02.y1 Sugano mouse liver mlia Mus musculus cDNA clone			02-SEP-1998
	IMAGE:1499714_5, similar to TR:019103 019103			
	INDP:ELUCRONS05V1TRANSFRASE ; mRNA sequence.			

Qy	241	caggacagaacagagaagaataat-----ttgttgacctgaactctgaatgtc	291
Db	269	TATGAATCGAGACAGCTGAGAATCCTTTAAATGAGATTGCAAATCTAGCTGTGAATGTC	328
Qy	292	ttagcaggcttacaaccctggcaatcagttataaaattaaatgatttttttgttaaata	351
Db	329	ATTCCAAACCCTGTCAGTGTGGGAAGCAGCAAAAACATTACAAGACTTCCTTCTTCAAATA	388
Qy	352	aggggaactttaaaaatgatgtgtgagagcttatcacaaatcaaacacacttatgaagaag	411
Db	389	ACTGGAGATTTTGAAAGTATTGTAGGAGTGTAATTGTACAACACAGNAATTCATGACCAAG	448
Qy	412	ctacaggaaccaactcacgatgaacgccttatagaccctgtgattccccgtggagacotg	471
Db	449	CTACGNATGCACAAATATGATTTAGTGTGGTATTAGACCCCTGTCGTTCCTGTGGAGAGTTG	508
Qy	472	atggctgagtgtctccagtccectttgtgctcacactta	511
Db	509	GTTGGCAGAAGTGCTTCAGATCCCCTTTTCGTATACACACTGA	548

RESULT	6	
LOCUS	AW012524	
DEFINITION	uc06a07.y1 Sugano mouse liver m1ia Mus musculus cDNA clone	10-SEP-1999
SEQUENCE	IMAGE:582580 5' similar to SW:UDBG.RABIT O19103	EST
VERSION	UDP-GLUCURONOSYLTRANSFERASE 2B16 PRECURSOR, MICROSOMAL ; , mRNA	
KEYWORDS	sequence.	
ACCESSION	AW012524	
VERSION	AW012524.1	GI:5861302
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 529) Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person, B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter, E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.	
TITLE	The WashU-NCI Mouse EST Project 1999	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810	

RESULT	7
AQ371717/c	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

MG1:930052
Seq primer: custom primer used
High quality sequence stop: 458.

1. .777

Location/Qualifiers
1. .601

/lab_host="DH10B"
/note=organ:kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGATGG); Site_2: DraIII (.ACCATGTG); 1st strand cDNA
(CACTGATGG)
was primed with an oligo(dT) primer
[ATGGCGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGGGCCACTG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGATGG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTGTCCTAAAGCTGCG and 3' end
primer CGAAGCTGCAGCTCGAGACA."

Query Match	22.7%	Score 162.6;	DI: 16;	Length 777;
Best Local Similarity	54.2%;	Pred. NO. 7.3e-35;		
Matches 378; Conservative	0;	Mismatches 309;	Indels 10;	Gaps 2;

Query Match	22.7%	Score 162.6;	DR 16;	Length 777;
Best Local Similarity	54.2%;	pred. No. 7.3e-35;		
Matches 378; Conservative	0;	Mismatches 309;	Indels 10;	Gaps

Qy

29 ttctgtcctcgagctcttctgtagtggtggattctataggaaagtccgtggtgcc 88
||||||| || | ||||| ||||| |||||
74 tcaactgcacaccacacctccccttttcgaatactggccaagtgctgggtggcc 133

[illegible]

Db	134	CAATGGATTTCAGCCATTGCTCAACTTGAAGACAAATCCAGACGAGGCTTCTGAAGAAGG	197
Qy	149	gcgatgaggtaacagtattgactcaactcaaacgcttcgttaattgactacaggagcctt	208

Db	194	GT	CGATGAAGT	GATGGTTC	TGAGACCTT	CAGCATCCTT	ATTCCTTATGAGGTTGACACACAT	253
Qv	209	ctgcattg	aaatttgagggtg	gtgtccat	tatgccacaggacag	aacagagaaaaatg	aaat--	266

Db 254 CTGCTATTGAATTCGAGACTTATCTACATCATACTCTCTTATCTGAGTTAGAGGAATTT 313

Db 314 TCTGGGAATCACTCAAGAAATATATTATGACTGCCAAGAGAGTCATTTTGGGGATACT 373

Qy 320 ttataaaatt-aattgatttttttttgataaagggaacctttataaataatgatgtgtgag 376
Db 374 TCCTAATGTTGCAAGAAATGGTTGGGTAGATTCAAAATATTTTGAAGTCTCTGTAA 433

QY 379 agctttatctacaatcagacacacttatgaagaagctacagcttaccacactcagatgtaacg 438
db 434 GATGTAGTGTTTTACAAAGAAGCTCATGACAAAGCTACAAATATCTCAAGGTTTGATGTGATC 493

QY 439 cttatagacctgtgattccocgtggagacctgatggctgaattgcttccagtcaccttt 498
 404 cttccacacatcccttcataccctgcggcgatctgctggctgagggtctcaagatcccccct 553

[illegible]

Db 554 GTGTACAGTCTACGCTTCTTCTCTGGCTCCACTTATGAGNAGTACAGTGGGGGACATCCCA
QY 559 gctccactttctctatgtacctgtgcctatgacaggactatcacgacagaatgacctttctg 618

Db 614 CTGCTACTTCTCATGTGGCCGTGTTGTTATGTCAGAAATTGAATGCAGAGATGACATTTTCATG 673

Qy 619 gaaagagtataaaaaatcaactcttcaggttgttccactctcaggattcaggattcacgac 678
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 674 GATAGGCTGAGAATGCCATCATATGCTGTGTGTTTGACTTTTGGTCTCCAACATTTTAT 733
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 679 tateattttgggaagaagatttatagtaagsgcatag 715
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 734 GAGAAGAACTGGAATCAGCTTTATACTGAAGTTTAAG 770
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9

AK004971 2573 bp mRNA HTC 08-FEB-2001

LOCUS Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:I30001D20, full insert sequence.

DEFINITION AK004971

ACCESSION AK004971.1 GI:12836559

VERSION CAP trapper.

KEYWORDS Mus musculus

SOURCE Mus musculus (strain:C57BL/6J) adult male liver cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library clone:I30001D20.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (sites)

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

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REFERENCE 2 (sites)

AUTHORS Carninci,P., Shibata,Y., Hayata,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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MEDLINE 204939374

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AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Kikuchi,N., Ishii.Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanahi,M., Yoneda,Y., Ishikawa,T., Ozawa.K., Tanaka,T., Matsura.S., Okazaki,Y., Muramatsu.M., Inoue,Y. and Hayashizaki,Y.

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AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.

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REFERENCE 5 (bases 1 to 2573)

AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanaoka,T., Hara.A., Hayatsu,N., Hiramoto,K., Hiraoka.T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato.H., Kawai.J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi.K., Nomura,K., Numazaki,R., Ohno.M., Okazaki,Y., Okido,T., Owa.C., Saïto,H., Saïto.R., Sakai,C., Sakai,K., Sano.H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki.H., Tagami.M., Tagawa,A., Takahashi,F., Tanaka,T., Teijma.Y., Toya.T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino.M., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp). URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

[illegible]

Qy 649 ttgttccacttctggattcag 669
| | | | | | | | | |
Db 687 TACTTGCACFTTGGGTCAG 707

Search completed: August 27, 2001, 17:07:48
Job time: 9716 sec

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